

# RAW SEQUENCE LISTING

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Application Serial Number: 10/699,035B  
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IFW16

**RAW SEQUENCE LISTING**  
**PATENT APPLICATION: US/10/699,035B**

**DATE: 10/06/2006**  
**TIME: 10:14:04**

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4 <110> APPLICANT: BATEMAN, JOHN
5   FITZGERALD, DAVID
7 <120> TITLE OF INVENTION: A MOLECULAR MARKER
9 <130> FILE REFERENCE: 071838.0142
11 <140> CURRENT APPLICATION NUMBER: 10/699,035B
12 <141> CURRENT FILING DATE: 2003-10-31
14 <150> PRIOR APPLICATION NUMBER: PCT/AU02/00542
15 <151> PRIOR FILING DATE: 2002-05-02
17 <150> PRIOR APPLICATION NUMBER: AU PR4701/01
18 <151> PRIOR FILING DATE: 2001-05-02
20 <160> NUMBER OF SEQ ID NOS: 41
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25 <211> LENGTH: 537
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36 ccccccattgc aggagctcaa ggacctggc gtcacccgtgt tcattgtcag caccggccga 420
37 ggcaacttcc tggagctgtc agccgctgcc tcagccccgt ccgagaagca cctgcacttt 480
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49 Tyr Glu Phe Ser Arg Val Arg Glu Phe Val Gly Gln Leu Val Ala Pro
50       20          25          30
52 Leu Pro Leu Gly Thr Gly Ala Leu Arg Ala Ser Leu Val His Val Gly
53       35          40          45
55 Ser Arg Pro Tyr Thr Glu Phe Pro Phe Gly Gln His Ser Ser Gly Glu
56       50          55          60
58 Ala Ala Gln Asp Ala Val Arg Ala Ser Ala Gln Arg Met Gly Asp Thr
59       65          70          75          80
61 His Thr Gly Leu Ala Leu Val Tyr Ala Lys Glu Gln Leu Phe Ala Glu
62       85          90          95

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 68 115 120 125  
 70 Asp Leu Gly Val Thr Val Phe Ile Val Ser Thr Gly Arg Gly Asn Phe  
 71 130 135 140  
 73 Leu Glu Leu Ser Ala Ala Ser Ala Pro Ala Glu Lys His Leu His  
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 91 agctcagcca gcgtgtcaca ctatgagttc tcaagagttc gggaaatttggtt ggggcagctg 180  
 92 gtggctacga tgtctttcgg accccggggct ctgcgtgcta gtctggtgca cgtgggcagc 240  
 93 cagcctcaca cagagtttac ttttggaccag tacagttcag gccaggctat acgggatgcc 300  
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 95 aaagaacaat tggttgctga ggaagcaggt gcccggccag gggttcccaa ggtgctggtg 420  
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 121 Leu Ala Arg Ser Ser Ile Glu Arg Gly Ser Thr Ala Ser Asp Pro Gln  
 122 20 25 30  
 124 Gly Asp Leu Leu Phe Leu Leu Asp Ser Ser Ala Ser Val Ser His Tyr

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131	65	70	75
133	80		
134	Gln Pro His Thr Glu Phe Thr Phe Asp Gln Tyr Ser Ser Gly Gln Ala		
136	85	90	95
136	Ile Arg Asp Ala Ile Arg Val Ala Pro Gln Arg Met Gly Asp Thr Asn		
137	100	105	110
139	Thr Gly Leu Ala Leu Ala Tyr Ala Lys Glu Gln Leu Phe Ala Glu Glu		
140	115	120	125
142	Ala Gly Ala Arg Pro Gly Val Pro Lys Val Leu Val Trp Val Thr Asp		
143	130	135	140
145	Gly Gly Ser Ser Asp Pro Val Gly Pro Pro Met Gln Glu Leu Lys Asp		
146	145	150	155
148	160		
149	Leu Gly Val Thr Ile Phe Ile Val Ser Thr Gly Arg Gly Asn Leu Leu		
151	165	170	175
151	Glu Leu Leu Ala Ala Ala Ser Ala Pro Ala Glu Lys His Leu His Phe		
152	180	185	190
154	Val Asp Val Asp Asp Leu Pro Ile Ile Ala Arg Glu Leu Arg Gly Ser		
155	195	200	205
157	160		
157	Ile Thr Asp Ala Met Gln Pro Gln Gln Leu His Ala Ser Glu Val Leu		
158	210	215	220
160	165		
160	Ser Ser Gly Phe Arg Leu Ser Trp Pro Pro Leu Leu Thr Ala Asp Ser		
161	225	230	235
163	240		
163	Gly Tyr Tyr Val Leu Glu Leu Val Pro Ser Gly Lys Leu Ala Thr Thr		
164	245	250	255
166	165		
166	Arg Arg Gln Gln Leu Pro Gly Asn Ala Thr Ser Trp Thr Trp Thr Asp		
167	260	265	270
169	170		
169	Leu Asp Pro Asp Thr Asp Tyr Glu Val Ser Leu Leu Pro Glu Ser Asn		
170	275	280	285
172	171		
172	Val His Leu Leu Arg Pro Gln His Val Arg Val Arg Thr Leu Gln Glu		
173	290	295	300
175	176		
175	Glu Ala Gly Pro Glu Arg Ile Val Ile Ser His Ala Arg Pro Arg Ser		
176	305	310	315
178	177		
178	Leu Arg Val Ser Trp Ala Pro Ala Leu Gly Pro Asp Ser Ala Leu Gly		
179	325	330	335
181	180		
181	Tyr His Val Gln Leu Gly Pro Leu Gln Gly Ser Leu Glu Arg Val		
182	340	345	350
184	183		
184	Glu Val Pro Ala Gly Gln Asn Ser Thr Thr Val Gln Gly Leu Thr Pro		
185	355	360	365
187	186		
187	Cys Thr Thr Tyr Leu Val Thr Val Thr Ala Ala Phe Arg Ser Gly Arg		
188	370	375	380
190	189		
190	Gln Arg Ala Leu Ser Ala Lys Ala Cys Thr Ala Ser Gly Ala Arg Thr		
191	385	390	395
193	192		
193	Arg Ala Pro Gln Ser Met Arg Pro Glu Ala Gly Pro Arg Glu Pro		
194	405	410	415
197	<210> SEQ ID NO: 5		
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199 <212> TYPE: DNA  
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 205 agctcagcca gcgttctca ctacgagttc tccccgggttc gggagttgt gggcagctg 180  
 206 gtggctccac tgccccctggg cacccggggc ctgcgtgcca gtctggtgc cgtggcagt 240  
 207 cggccataca ccgagttccc ttccggccag cacagctgg gtgaggctgc ccaggatgcg 300  
 208 gtgcgtgctt ctgcccagcg catgggtgac acccacactg gcctggcgct ggtctatgcc 360  
 209 aaggaacagc tgtttgcgtga agcatcaggt gcccgccag gggtgccaa agtgtctggtg 420  
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 211 ctgggcgtca ccgtgttcat tgtcagcacc ggccgaggca acttccttgc gctgtcagcc 540  
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 213 attgtccaag agctgagggg ctccattctc gcgtgcggc cgcagcact ccatgccacg 660  
 214 gagatcacgt ccagccggctt cccctggcc tggccaccccccc tgctgaccgc agactcgggc 720  
 215 tactatgtgc tggagctggt gcccagcgcc cagccggggg ctgcaagacg ccagcagctg 780  
 216 ccagggaaacg ccacggactg gatctggggc gcctcgacc cggacacgga ctacgacgtg 840  
 217 gcgttagtgc ctgagtc当地 cgtgcgc当地 ctgaggcccccc agatcctgcg ggtgcgcacg 900  
 218 cggccagagg aggccggggcc agagcgc当地 gtcatctccc acgccccggcc ggcagcctc 960  
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 221 acgctgc当地 ggctggccggcc gggcaccggc tacctggta ccgtgaccgc cgccctccgc 1140  
 222 tcggccgc当地 agagcgc当地 gtccgc当地 ag gctgc当地 cgc当地 ggc当地 1200  
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 234 Leu Ala Arg Ser Gly Ala Glu Arg Gly Pro Pro Ala Ser Ala Pro Arg  
 235 20 25 30  
 237 Gly Asp Leu Met Phe Leu Leu Asp Ser Ser Ala Ser Val Ser His Tyr  
 238 35 40 45  
 240 Glu Phe Ser Arg Val Arg Glu Phe Val Gly Gln Leu Val Ala Pro Leu  
 241 50 55 60  
 243 Pro Leu Gly Thr Gly Ala Leu Arg Ala Ser Leu Val His Val Gly Ser  
 244 65 70 75 80  
 246 Arg Pro Tyr Thr Glu Phe Pro Phe Gly Gln His Ser Ser Gly Glu Ala  
 247 85 90 95  
 249 Ala Gln Asp Ala Val Arg Ala Ser Ala Gln Arg Met Gly Asp Thr His  
 250 100 105 110  
 252 Thr Gly Leu Ala Leu Val Tyr Ala Lys Glu Gln Leu Phe Ala Glu Ala  
 253 115 120 125  
 255 Ser Gly Ala Arg Pro Gly Val Pro Lys Val Leu Val Trp Val Thr Asp  
 256 130 135 140  
 258 Gly Gly Ser Ser Asp Pro Val Gly Pro Pro Met Gln Glu Leu Lys Asp  
 259 145 150 155 160

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261 Leu Gly Val Thr Val Phe Ile Val Ser Thr Gly Arg Gly Asn Phe Leu  
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 265       180           185           190  
 267 Val Asp Val Asp Asp Leu His Ile Ile Val Gln Glu Leu Arg Gly Ser  
 268       195           200           205  
 270 Ile Leu Asp Ala Met Arg Pro Gln Gln Leu His Ala Thr Glu Ile Thr  
 271       210           215           220  
 273 Ser Ser Gly Phe Arg Leu Ala Trp Pro Pro Leu Leu Thr Ala Asp Ser  
 274 225           230           235           240  
 276 Gly Tyr Tyr Val Leu Glu Leu Val Pro Ser Ala Gln Pro Gly Ala Ala  
 277       245           250           255  
 279 Arg Arg Gln Gln Leu Pro Gly Asn Ala Thr Asp Trp Ile Trp Ala Gly  
 280       260           265           270  
 282 Leu Asp Pro Asp Thr Asp Tyr Asp Val Ala Leu Val Pro Glu Ser Asn  
 283       275           280           285  
 285 Val Arg Leu Leu Arg Pro Gln Ile Leu Arg Val Arg Thr Arg Pro Glu  
 286       290           295           300  
 288 Glu Ala Gly Pro Glu Arg Ile Val Ile Ser His Ala Arg Pro Arg Ser  
 289 305           310           315           320  
 291 Leu Arg Val Ser Trp Ala Pro Ala Leu Gly Ser Ala Ala Ala Leu Gly  
 292       325           330           335  
 294 Tyr His Val Gln Phe Gly Pro Leu Arg Gly Gly Glu Ala Gln Arg Val  
 295       340           345           350  
 297 Glu Val Pro Ala Gly Arg Asn Cys Thr Thr Leu Gln Gly Leu Ala Pro  
 298       355           360           365  
 300 Gly Thr Ala Tyr Leu Val Thr Val Thr Ala Ala Phe Arg Ser Gly Arg  
 301       370           375           380  
 303 Glu Ser Ala Leu Ser Ala Lys Ala Cys Thr Pro Asp Gly Pro Arg Pro  
 304 385           390           395           400  
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 321 gtgctagtct ggtcacgtg ggcagccagc ctcacacaga gtttacttt gaccagtaca 180  
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 325 gccccccat gcaggagctc aaggacctgg gtgtcaccat cttcattgtc agcaactggcc 420  
 326 gaggcaacct gttggagctg ttggcagctg cctcggctcc tgccgagaag caccctacact 480  
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**VERIFICATION SUMMARY**

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